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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2011; month=5; day=9; hr=12; min=37; sec=34; ms=552;]

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Application No: 08963656 Version No: 2.0

Input Set:

Output Set:

Started: 2011-05-06 10:32:16.872
Finished: 2011-05-06 10:32:19.024
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 152 ms
Total Warnings: 14
Total Errors: 5
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

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SEQUENCE LISTING

<110> GERARD, CRAIG J.
GERARD, NORMA P.
MACKAY, CHARLES R.
PONATH, PAUL D.
POST, THEODORE W.
QIN, SHIXIN

<120> ANTIBODIES TO C-C CHEMOKINE RECEPTOR 3 PROTEIN

<130> 079259-0040

<140> 08963656
<141> 1997-11-03

<150> 08/720,565
<151> 1996-09-30

<150> PCT/US96/00608
<151> 1996-01-19

<150> 08/375,199
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Leu Leu Gly Asn Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
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Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
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Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
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His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
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Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
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Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
145 150 155 160

Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
165 170 175

Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
180 185 190

Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
195 200 205

Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
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Thr Leu Leu Arg Cys Pro Ser Lys Lys Tyr Lys Ala Ile Arg Leu
225 230 235 240

Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
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Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
260 265 270

Cys Glu Arg Thr Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
275 280 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
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Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
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Met Thr Thr Ser Leu Asp Thr
1 5

gtt gag acc ttt ggt acc aca tcc tac tat gat gac gtg ggc ctg ctc 160
Val Glu Thr Phe Gly Thr Ser Tyr Tyr Asp Asp Val Gly Leu Leu
10 15 20

tgt gaa aaa gct gat acc aga gca ctg atg gcc cag ttt gtg ccc ccg 208
Cys Glu Lys Ala Asp Thr Arg Ala Leu Met Ala Gln Phe Val Pro Pro
25 30 35

ctg tac tcc ctg gtg ttc act gtg ggc ctc ttg ggc aat gtg gtg gtg 256
Leu Tyr Ser Leu Val Phe Thr Val Gly Leu Leu Gly Asn Val Val Val
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gtg atg atc ctc ata aaa tac agg agg ctc cga att atg acc aac atc Val Met Ile Leu Ile Lys Tyr Arg Arg Leu Arg Ile Met Thr Asn Ile	60	65	70	304	
tac ctg ctc aac ctg gcc att tcg gac ctg ctc ttc ctc gtc acc ctt Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Val Thr Leu	75	80	85	352	
cca ttc tgg atc cac tat gtc agg ggg cat aac tgg gtt ttt ggc cat Pro Phe Trp Ile His Tyr Val Arg Gly His Asn Trp Val Phe Gly His	90	95	100	400	
ggc atg tgt aag ctc ctc tca ggg ttt tat cac aca ggc ttg tac agc Gly Met Cys Lys Leu Leu Ser Gly Phe Tyr His Thr Gly Leu Tyr Ser	105	110	115	448	
gag atc ttt ttc ata atc ctg ctg aca atc gac agg tac ctg gcc att Glu Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile	120	125	130	135	496
gtc cat gct gtg ttt gcc ctt cga gcc cg act gtc act ttt ggt gtc Val His Ala Val Phe Ala Leu Arg Ala Arg Thr Val Thr Phe Gly Val	140	145	150	544	
atc acc agc atc gtc acc tgg ggc ctg gca gtg cta gca gct ctt cct Ile Thr Ser Ile Val Thr Trp Gly Leu Ala Val Leu Ala Ala Leu Pro	155	160	165	592	
gaa ttt atc ttc tat gag act gaa gag ttg ttt gaa gag act ctt tgc Glu Phe Ile Phe Tyr Glu Thr Glu Glu Leu Phe Glu Glu Thr Leu Cys	170	175	180	640	
agt gct ctt tac cca gag gat aca gta tat agc tgg agg cat ttc cac Ser Ala Leu Tyr Pro Glu Asp Thr Val Tyr Ser Trp Arg His Phe His	185	190	195	688	
act ctg aga atg acc atc ttc tgt ctc gtt ctc cct ctg ctc gtt atg Thr Leu Arg Met Thr Ile Phe Cys Leu Val Leu Pro Leu Leu Val Met	200	205	210	215	736
gcc atc tgc tac aca gga atc atc aaa acg ctg ctg agg tgc ccc agt Ala Ile Cys Tyr Thr Gly Ile Ile Lys Thr Leu Leu Arg Cys Pro Ser	220	225	230	784	
aaa aaa aag tac aag gcc atc cgg ctc att ttt gtc atc atg gcg gtg Lys Lys Lys Tyr Lys Ala Ile Arg Leu Ile Phe Val Ile Met Ala Val	235	240	245	832	
ttt ttc att ttc tgg aca ccc tac aat gtg gct atc ctt ctc tct tcc Phe Phe Ile Phe Trp Thr Pro Tyr Asn Val Ala Ile Leu Leu Ser Ser	250	255	260	880	
tat caa tcc atc tta ttt gga aat gac tgt gag cgg agc aag cat ctg Tyr Gln Ser Ile Leu Phe Gly Asn Asp Cys Glu Arg Ser Lys His Leu	265	270	275	928	
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Asp Leu Val Met Leu Val Thr Glu Val Ile Ala Tyr Ser His Cys Cys
280 285 290 295

atg aac ccg gtg atc tac gcc ttt gtt gga gag agg ttc cgg aag tac 1024
Met Asn Pro Val Ile Tyr Ala Phe Val Gly Glu Arg Phe Arg Lys Tyr
300 305 310

ctg cgc cac ttc ttc cac agg cac ttg ctc atg cac ctg ggc aga tac 1072
Leu Arg His Phe Phe His Arg His Leu Leu Met His Leu Gly Arg Tyr
315 320 325

atc cca ttc ctt cct agt gag aag ctg gaa aga acc agc tct gtc tct 1120
Ile Pro Phe Leu Pro Ser Glu Lys Leu Glu Arg Thr Ser Ser Val Ser
330 335 340

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Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
35 40 45

Leu Leu Gly Asn Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80

Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
85 90 95

His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr

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120

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Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
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Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
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Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
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Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
180 185 190

Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
195 200 205

Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220

Thr Leu Leu Arg Cys Pro Ser Lys Lys Tyr Lys Ala Ile Arg Leu
225 230 235 240

Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
245 250 255

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
260 265 270

Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
275 280 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305 310 315 320

Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
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Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
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Ile Val Phe

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tttgtcccccc gctgtactcc ctgggtgtca ctgtgggcctt cttggcaat gtggtggtgg 180

tgtatgatcct cataaaaatac aggaggctcc gaattatgac caacatctac ctgctcaacc 240

tggccatttc ggacctgctc ttccctcgta cccttccattt ctggatccac tatgtcagg 300

ggcataactg ggttttggc catggcatgt gtaagcttctt ctcagggtttt tatacacacag 360

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aggccatccg gctcattttt gtcataatgg cggtgtttttt cattttctgg acaccctaca 780

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tgaacccgggt gatctacgcc tttgttggag agaggttccg gaagtacctg cgccacttst 960

tccacaggca cttgctcatg cacctggca gatacatccc attccttctt agtgagaagc 1020

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Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
35 40 45

Leu Leu Gly Asn Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80

Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
85 90 95

His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Ph